

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/575,192
Source: IFWP
Date Processed by STIC: 04/24/2006

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 04/24/2006

PATENT APPLICATION: US/10/575,192

TIME: 16:12:56

Input Set : A:\14875-159US1.txt

Output Set: N:\CRF4\04242006\J575192.raw

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3 <110> APPLICANT: Igawa, Tomoyuki
4     Sekimori, Yasuo
6 <120> TITLE OF INVENTION: IgM high concentration stabilized solution
8 <130> FILE REFERENCE: 14875-159US1
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/575,192
C--> 10 <141> CURRENT FILING DATE: 2006-04-07
10 <150> PRIOR APPLICATION NUMBER: PCT/JP2004/14935
11 <151> PRIOR FILING DATE: 2004-10-08
13 <150> PRIOR APPLICATION NUMBER: JP 2003-351388
14 <151> PRIOR FILING DATE: 2003-10-09
16 <160> NUMBER OF SEQ ID NOS: 18
18 <170> SOFTWARE: PatentIn version 3.1
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 1779
22 <212> TYPE: DNA
23 <213> ORGANISM: Homo sapiens
25 <220> FEATURE:
26 <221> NAME/KEY: CDS
27 <222> LOCATION: (1)..(1779)
28 <223> OTHER INFORMATION:
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31 atg gag ttt ggg ctg agc tgg ctt ttt ctt gtg gct att tta aaa ggt      48
32 Met Glu Phe Gly Leu Ser Trp Leu Phe Leu Val Ala Ile Leu Lys Gly
33 1          5          10          15
35 gtc cag tgt gag gtg cag ctg ttg gat tct ggg gga ggc ttg gta cag      96
36 Val Gln Cys Glu Val Gln Leu Leu Asp Ser Gly Gly Gly Leu Val Gln
37          20          25          30
39 cct ggg ggg tgc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttt      144
40 Pro Gly Gly Cys Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
41          35          40          45
43 agc agc tgt gcc atg agc tgg gtc cgc cag gct cca ggg aag ggg ctg      192
44 Ser Ser Cys Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
45          50          55          60
47 gag tgg gtc tca gct att agt ggt agt ggt ggt agc aca tac tac gca      240
48 Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala
49 65          70          75          80
51 gac tcc gtg aag ggc cgg ttc acc atc tcc aga gac aaa tcc aag aac      288
52 Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Lys Ser Lys Asn
53          85          90          95
55 acg ttg tat ctg caa atg aac agc ctg aga gcc gag gac acg gcc gta      336
56 Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
57          100         105         110
59 tat tac tgt gcg aaa ggt ggc aac gat att ttg act ggt tat tat gct      384

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60	Tyr	Tyr	Cys	Ala	Lys	Gly	Gly	Asn	Asp	Ile	Leu	Thr	Gly	Tyr	Tyr	Ala	
61			115					120					125				
63	tgg	ggc	cag	gga	acc	ctg	gtc	acc	gtc	tcc	tca	ggg	agt	gca	tcc	gcc	432
64	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Gly	Ser	Ala	Ser	Ala	
65		130					135					140					
67	cca	acc	ctt	ttc	ccc	ctc	gtc	tcc	tgt	gag	aat	tcc	ccg	tcg	gat	acg	480
68	Pro	Thr	Leu	Phe	Pro	Leu	Val	Ser	Cys	Glu	Asn	Ser	Pro	Ser	Asp	Thr	
69	145					150				155					160		
71	agc	agc	gtg	gcc	gtt	ggc	tgc	ctc	gca	cag	gac	ttc	ctt	ccc	gac	tcc	528
72	Ser	Ser	Val	Ala	Val	Gly	Cys	Leu	Ala	Gln	Asp	Phe	Leu	Pro	Asp	Ser	
73				165						170					175		
75	atc	act	ttc	tcc	tgg	aaa	tac	aag	aac	aac	tct	gac	atc	agc	agc	acc	576
76	Ile	Thr	Phe	Ser	Trp	Lys	Tyr	Lys	Asn	Asn	Ser	Asp	Ile	Ser	Ser	Thr	
77			180						185				190				
79	cgg	ggc	ttc	cca	tca	gtc	ctg	aga	ggg	ggc	aag	tac	gca	gcc	acc	tca	624
80	Arg	Gly	Phe	Pro	Ser	Val	Leu	Arg	Gly	Gly	Lys	Tyr	Ala	Ala	Thr	Ser	
81			195				200					205					
83	cag	gtg	ctg	ctg	cct	tcc	aag	gac	gtc	atg	cag	ggc	aca	gac	gaa	cac	672
84	Gln	Val	Leu	Leu	Pro	Ser	Lys	Asp	Val	Met	Gln	Gly	Thr	Asp	Glu	His	
85		210				215					220						
87	gtg	gtg	tgc	aaa	gtc	cag	cac	ccc	aac	ggc	aac	aaa	gaa	aag	aac	gtg	720
88	Val	Val	Cys	Lys	Val	Gln	His	Pro	Asn	Gly	Asn	Lys	Glu	Lys	Asn	Val	
89	225				230				235				240				
91	cct	ctt	cca	gtg	att	gct	gag	ctg	cct	ccc	aaa	gtg	agc	gtc	ttc	gtc	768
92	Pro	Leu	Pro	Val	Ile	Ala	Glu	Leu	Pro	Pro	Lys	Val	Ser	Val	Phe	Val	
93				245					250				255				
95	cca	ccc	cgc	gac	ggc	ttc	ttc	ggc	aac	ccc	cgc	aag	tcc	aag	ctc	atc	816
96	Pro	Pro	Arg	Asp	Gly	Phe	Phe	Gly	Asn	Pro	Arg	Lys	Ser	Lys	Leu	Ile	
97			260				265				270						
99	tgc	cag	gcc	acg	ggt	ttc	agt	ccc	cgg	cag	att	cag	gtg	tcc	tgg	ctg	864
100	Cys	Gln	Ala	Thr	Gly	Phe	Ser	Pro	Arg	Gln	Ile	Gln	Val	Ser	Trp	Leu	
101			275				280					285					
103	cgc	gag	ggg	aag	cag	gtg	ggg	tct	ggc	gtc	acc	acg	gac	cag	gtg	cag	912
104	Arg	Glu	Gly	Lys	Gln	Val	Gly	Ser	Gly	Val	Thr	Thr	Asp	Gln	Val	Gln	
105		290				295					300						
107	gct	gag	gcc	aaa	gag	tct	ggg	ccc	acg	acc	tac	aag	gtg	acc	agc	aca	960
108	Ala	Glu	Ala	Lys	Glu	Ser	Gly	Pro	Thr	Thr	Tyr	Lys	Val	Thr	Ser	Thr	
109	305				310				315				320				
111	ctg	acc	atc	aaa	gag	agc	gac	tgg	ctc	ggc	cag	agc	atg	ttc	acc	tgc	1008
112	Leu	Thr	Ile	Lys	Glu	Ser	Asp	Trp	Leu	Gly	Gln	Ser	Met	Phe	Thr	Cys	
113				325					330				335				
115	cgc	gtg	gat	cac	agg	ggc	ctg	acc	ttc	cag	cag	aat	gcg	tcc	tcc	atg	1056
116	Arg	Val	Asp	His	Arg	Gly	Leu	Thr	Phe	Gln	Gln	Asn	Ala	Ser	Ser	Met	
117			340				345				350						
119	tgt	gtc	ccc	gat	caa	gac	aca	gcc	atc	cgg	gtc	ttc	gcc	atc	ccc	cca	1104
120	Cys	Val	Pro	Asp	Gln	Asp	Thr	Ala	Ile	Arg	Val	Phe	Ala	Ile	Pro	Pro	
121			355				360				365						
123	tcc	ttt	gcc	agc	atc	ttc	ctc	acc	aag	tcc	acc	aag	ttg	acc	tgc	ctg	1152
124	Ser	Phe	Ala	Ser	Ile	Phe	Leu	Thr	Lys	Ser	Thr	Lys	Leu	Thr	Cys	Leu	

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125      370      375      380
127 gtc aca gac ctg acc acc tat gac agc gtg acc atc tcc tgg acc cgc      1200
128 Val Thr Asp Leu Thr Thr Tyr Asp Ser Val Thr Ile Ser Trp Thr Arg
129 385      390      395      400
131 cag aat ggc gaa gct gtg aaa acc cac acc aac atc tcc gag agc cac      1248
132 Gln Asn Gly Glu Ala Val Lys Thr His Thr Asn Ile Ser Glu Ser His
133      405      410      415
135 ccc aat gcc act ttc agc gcc gtg ggt gag gcc agc atc tgc gag gat      1296
136 Pro Asn Ala Thr Phe Ser Ala Val Gly Glu Ala Ser Ile Cys Glu Asp
137      420      425      430
139 gac tgg aat tcc ggg gag agg ttc acg tgc acc gtg acc cac aca gac      1344
140 Asp Trp Asn Ser Gly Glu Arg Phe Thr Cys Thr Val Thr His Thr Asp
141      435      440      445
143 ctg ccc tcg cca ctg aag cag acc atc tcc cgg ccc aag ggg gtg gcc      1392
144 Leu Pro Ser Pro Leu Lys Gln Thr Ile Ser Arg Pro Lys Gly Val Ala
145      450      455      460
147 ctg cac agg ccc gat gtc tac ttg ctg cca cca gcc cgg gag cag ctg      1440
148 Leu His Arg Pro Asp Val Tyr Leu Leu Pro Pro Ala Arg Glu Gln Leu
149 465      470      475      480
151 aac ctg cgg gag tcg gcc acc atc acg tgc ctg gtg acg ggc ttc tct      1488
152 Asn Leu Arg Glu Ser Ala Thr Ile Thr Cys Leu Val Thr Gly Phe Ser
153      485      490      495
155 ccc gcg gac gtc ttc gtg cag tgg atg cag agg ggg cag ccc ttg tcc      1536
156 Pro Ala Asp Val Phe Val Gln Trp Met Gln Arg Gly Gln Pro Leu Ser
157      500      505      510
159 ccg gag aag tat gtg acc agc gcc cca atg cct gag ccc cag gcc cca      1584
160 Pro Glu Lys Tyr Val Thr Ser Ala Pro Met Pro Glu Pro Gln Ala Pro
161      515      520      525
163 ggc cgg tac ttc gcc cac agc atc ctg acc gtg tcc gaa gag gaa tgg      1632
164 Gly Arg Tyr Phe Ala His Ser Ile Leu Thr Val Ser Glu Glu Glu Trp
165      530      535      540
167 aac acg ggg gag acc tac acc tgc gtg gtg gcc cat gag gcc ctg ccc      1680
168 Asn Thr Gly Glu Thr Tyr Thr Cys Val Val Ala His Glu Ala Leu Pro
169 545      550      555      560
171 aac agg gtc acc gag agg acc gtg gac aag tcc acc ggt aaa ccc acc      1728
172 Asn Arg Val Thr Glu Arg Thr Val Asp Lys Ser Thr Gly Lys Pro Thr
173      565      570      575
175 ctg tac aac gtg tcc ctg gtc atg tcc gac aca gct ggc acc tgc tac      1776
176 Leu Tyr Asn Val Ser Leu Val Met Ser Asp Thr Ala Gly Thr Cys Tyr
177      580      585      590
179 tga      1779
182 <210> SEQ ID NO: 2
183 <211> LENGTH: 592
184 <212> TYPE: PRT
185 <213> ORGANISM: Homo sapiens
187 <400> SEQUENCE: 2
188 Met Glu Phe Gly Leu Ser Trp Leu Phe Leu Val Ala Ile Leu Lys Gly
189 1      5      10      15
190 Val Gln Cys Glu Val Gln Leu Leu Asp Ser Gly Gly Gly Leu Val Gln

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191          20          25          30
192 Pro Gly Gly Cys Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
193          35          40          45
194 Ser Ser Cys Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
195          50          55          60
196 Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala
197 65          70          75          80
198 Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Lys Ser Lys Asn
199          85          90          95
200 Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
201          100         105         110
202 Tyr Tyr Cys Ala Lys Gly Gly Asn Asp Ile Leu Thr Gly Tyr Tyr Ala
203          115         120         125
204 Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Ser Ala Ser Ala
205          130         135         140
206 Pro Thr Leu Phe Pro Leu Val Ser Cys Glu Asn Ser Pro Ser Asp Thr
207 145         150         155         160
208 Ser Ser Val Ala Val Gly Cys Leu Ala Gln Asp Phe Leu Pro Asp Ser
209          165         170         175
210 Ile Thr Phe Ser Trp Lys Tyr Lys Asn Asn Ser Asp Ile Ser Ser Thr
211          180         185         190
212 Arg Gly Phe Pro Ser Val Leu Arg Gly Gly Lys Tyr Ala Ala Thr Ser
213          195         200         205
214 Gln Val Leu Leu Pro Ser Lys Asp Val Met Gln Gly Thr Asp Glu His
215          210         215         220
216 Val Val Cys Lys Val Gln His Pro Asn Gly Asn Lys Glu Lys Asn Val
217 225         230         235         240
218 Pro Leu Pro Val Ile Ala Glu Leu Pro Pro Lys Val Ser Val Phe Val
219          245         250         255
220 Pro Pro Arg Asp Gly Phe Phe Gly Asn Pro Arg Lys Ser Lys Leu Ile
221          260         265         270
222 Cys Gln Ala Thr Gly Phe Ser Pro Arg Gln Ile Gln Val Ser Trp Leu
223          275         280         285
224 Arg Glu Gly Lys Gln Val Gly Ser Gly Val Thr Thr Asp Gln Val Gln
225          290         295         300
226 Ala Glu Ala Lys Glu Ser Gly Pro Thr Thr Tyr Lys Val Thr Ser Thr
227 305         310         315         320
228 Leu Thr Ile Lys Glu Ser Asp Trp Leu Gly Gln Ser Met Phe Thr Cys
229          325         330         335
230 Arg Val Asp His Arg Gly Leu Thr Phe Gln Gln Asn Ala Ser Ser Met
231          340         345         350
232 Cys Val Pro Asp Gln Asp Thr Ala Ile Arg Val Phe Ala Ile Pro Pro
233          355         360         365
234 Ser Phe Ala Ser Ile Phe Leu Thr Lys Ser Thr Lys Leu Thr Cys Leu
235          370         375         380
236 Val Thr Asp Leu Thr Thr Tyr Asp Ser Val Thr Ile Ser Trp Thr Arg
237 385         390         395         400
238 Gln Asn Gly Glu Ala Val Lys Thr His Thr Asn Ile Ser Glu Ser His
239          405         410         415

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Output Set: N:\CRF4\04242006\J575192.raw

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240 Pro Asn Ala Thr Phe Ser Ala Val Gly Glu Ala Ser Ile Cys Glu Asp
241           420           425           430
242 Asp Trp Asn Ser Gly Glu Arg Phe Thr Cys Thr Val Thr His Thr Asp
243           435           440           445
244 Leu Pro Ser Pro Leu Lys Gln Thr Ile Ser Arg Pro Lys Gly Val Ala
245           450           455           460
246 Leu His Arg Pro Asp Val Tyr Leu Leu Pro Pro Ala Arg Glu Gln Leu
247 465           470           475           480
248 Asn Leu Arg Glu Ser Ala Thr Ile Thr Cys Leu Val Thr Gly Phe Ser
249           485           490           495
250 Pro Ala Asp Val Phe Val Gln Trp Met Gln Arg Gly Gln Pro Leu Ser
251           500           505           510
252 Pro Glu Lys Tyr Val Thr Ser Ala Pro Met Pro Glu Pro Gln Ala Pro
253           515           520           525
254 Gly Arg Tyr Phe Ala His Ser Ile Leu Thr Val Ser Glu Glu Glu Trp
255           530           535           540
256 Asn Thr Gly Glu Thr Tyr Thr Cys Val Val Ala His Glu Ala Leu Pro
257 545           550           555           560
258 Asn Arg Val Thr Glu Arg Thr Val Asp Lys Ser Thr Gly Lys Pro Thr
259           565           570           575
260 Leu Tyr Asn Val Ser Leu Val Met Ser Asp Thr Ala Gly Thr Cys Tyr
261           580           585           590

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264 <210> SEQ ID NO: 3

265 <211> LENGTH: 723

266 <212> TYPE: DNA

267 <213> ORGANISM: Homo sapiens

269 <220> FEATURE:

270 <221> NAME/KEY: CDS

271 <222> LOCATION: (1)..(723)

272 <223> OTHER INFORMATION:

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275 atg gtg ttg cag acc cag gtc ttc att tct ctg ttg ctc tgg atc tct      48
276 Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
277 1           5           10           15
279 ggt gcc tac ggg gac atc gtg atg acc cag tct cca gac tcc ctg gct      96
280 Gly Ala Tyr Gly Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala
281           20           25           30
283 gtg tct ctg ggc gag agg gcc acc atc aac tgc aag tcc agc cag agt      144
284 Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser
285           35           40           45
287 gtt tta tac agc tcc aac aat aag aac tac tta gct tgg tac cag cag      192
288 Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln
289           50           55           60
291 aaa cca gga cag cct cct aag ctg ctc att tac tgg gca tct acc cgg      240
292 Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
293 65           70           75           80
295 gaa tcc ggg gtc cct gac cga ttc agt ggc agc ggg tct ggg aca gat      288
296 Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
297           85           90           95

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RAW SEQUENCE LISTING ERROR SUMMARY

DATE: 04/24/2006

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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:7,8,9,10,11,12,13,14,15,16,17,18

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/575,192

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Input Set : A:\14875-159US1.txt

Output Set: N:\CRF4\04242006\J575192.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:30 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:28

L:274 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:272

L:386 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:384